SEQUENCE LISTING

<110> ALBERTSEN, MARC C.
      FOX, TIM
      HUFFMAN, GARY
      TRIMNELL, MARY

<120> NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
      METHOD OF USING SAME

<130> 1148

<140> 09/670,153
<141> 2000-09-26

<160> 7

<170> PatentIn Ver. 2.1

<210> 1
<211> 1906
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1..1638, 1642..1767)

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ttc ttc cca cta gca ggg cct cac aag tac atc gcg ctc ctt ctg gtt   96
Phe Phe Pro Leu Ala Gly Pro His Lys Tyr Ile Ala Leu Leu Leu Val
            20   25   30

gtc ctc tca tgg atc ctg gtc cag agg tgg agc ctg agg aag cag aaa   144
Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys
        35   40   45

ggc ccg aga tca tgg cca gtc atc ggc gca acg gtg gag cag ctg agg   192
Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg
    50   55   60

aac tac cac cgg atg cac gac tgg ctt gtc ggg tac ctg tca cgg cac   240
Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His
65   70   75   80

agg aca gtg acc gtc gac atg ccg ttc act tcc tac acc tac atc gct   288
Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala
                85   90   95

gac ccg gtg aat gtc gag cat gtc ctc aag act aac ttc acc aat tac   336
Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr
            100   105   110

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ccc aag gga atc gtg    c aga tcc tac atg gac gtg ctc ctc ggt gac        384
Pro Lys Gly Ile Val Tyr Arg Ser Tyr Met Asp Val Leu Leu Gly Asp
        115                 120                 125

ggc atc ttc aac gcc gac ggc gag ctg tgg agg aag cag agg aag acg        432
Gly Ile Phe Asn Ala Asp Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr
    130                 135                 140

gcg agt ttc gag ttc gcc tcc aag aac ctg agg gat ttc agc gcc att        480
Ala Ser Phe Glu Phe Ala Ser Lys Asn Leu Arg Asp Phe Ser Ala Ile
145                 150                 155                 160

gtg ttc aga gag tac tcc ctg aag ctg tcg ggt ata ctg agc cag gca        528
Val Phe Arg Glu Tyr Ser Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala
                165                 170                 175

tcc aag gca ggc aaa gtt gtg gac atg cag gaa ctt tac atg agg atg        576
Ser Lys Ala Gly Lys Val Val Asp Met Gln Glu Leu Tyr Met Arg Met
                180                 185                 190

acg ctg gac tcc atc tgc aag gtt ggg ttc ggg gtc gag atc ggc acg        624
Thr Leu Asp Ser Ile Cys Lys Val Gly Phe Gly Val Glu Ile Gly Thr
            195                 200                 205

ctg tcg cca gat ctc ccc gag aac agc ttc gcg cag gcg ttc gat gcc        672
Leu Ser Pro Asp Leu Pro Glu Asn Ser Phe Ala Gln Ala Phe Asp Ala
    210                 215                 220

gcc aac atc atc atc acg ctg cgg ttc atc gac ccg ctg tgg cgc atc        720
Ala Asn Ile Ile Ile Thr Leu Arg Phe Ile Asp Pro Leu Trp Arg Ile
225                 230                 235                 240

aag agg ttc ttc cac gtc ggg tca gag gcc ctc cta gcg cag agc atc        768
Lys Arg Phe Phe His Val Gly Ser Glu Ala Leu Leu Ala Gln Ser Ile
                245                 250                 255

aag ctc gtg gac gag ttc acc tac agc gtg atc cgc cgg agg aag gcc        816
Lys Leu Val Asp Glu Phe Thr Tyr Ser Val Ile Arg Arg Arg Lys Ala
                260                 265                 270

gag atc gtc gag gtc cgg gcc agc ggc aaa cag gag aag atg aag cac        864
Glu Ile Val Glu Val Arg Ala Ser Gly Lys Gln Glu Lys Met Lys His
            275                 280                 285

gac atc ctg tca cgg ttc atc gag ctg ggc gag gcc ggc gac gac ggc        912
Asp Ile Leu Ser Arg Phe Ile Glu Leu Gly Glu Ala Gly Asp Asp Gly
        290                 295                 300

ggc ggc ttc ggg gac gat aag agc ctc cgg gac gtg gtg ctc aac ttc        960
Gly Gly Phe Gly Asp Asp Lys Ser Leu Arg Asp Val Val Leu Asn Phe
305                 310                 315                 320

gtg atc gcc ggg cgg gac acg acg gcg acg acg ctg tcg tgg ttc acg       1008
Val Ile Ala Gly Arg Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Thr
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cac atg gcc atg tcc c    ccg gac gtg gcc gag aag ctg cgc cgc gag      1056
His Met Ala Met Ser His Pro Asp Val Ala Glu Lys Leu Arg Arg Glu
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ctg tgc gcg ttc gag gcg gag cgc gcg cgc gag gag ggc gtc acg ctc      1104
Leu Cys Ala Phe Glu Ala Glu Arg Ala Arg Glu Glu Gly Val Thr Leu
            355                 360                 365

gtg ctc tgc ggc ggc gct gac gcc gac gac aag gcg ttc gcc gcc cgc      1152
Val Leu Cys Gly Gly Ala Asp Ala Asp Asp Lys Ala Phe Ala Ala Arg
            370                 375                 380

gtg gcg cag ttc gcg ggc ctc ctc acc tac gac agc ctc ggc aag ctg      1200
Val Ala Gln Phe Ala Gly Leu Leu Thr Tyr Asp Ser Leu Gly Lys Leu
385                 390                 395                 400

gtc tac ctc cac gcc tgc gtc acc gag acg ctc cgc ctg tac ccc gcc      1248
Val Tyr Leu His Ala Cys Val Thr Glu Thr Leu Arg Leu Tyr Pro Ala
                405                 410                 415

gtc cct cag gac ccc aag ggg atc ctg gag gac gac gtg ctg ccg gac      1296
Val Pro Gln Asp Pro Lys Gly Ile Leu Glu Asp Asp Val Leu Pro Asp
                420                 425                 430

ggg acg aag gtg agg gcc ggc ggg atg gtg acg tac gtg ccc tac tcg      1344
Gly Thr Lys Val Arg Ala Gly Gly Met Val Thr Tyr Val Pro Tyr Ser
            435                 440                 445

atg ggg cgg atg gag tac aac tgg ggc ccc gac gcg gcg agc ttc cgg      1392
Met Gly Arg Met Glu Tyr Asn Trp Gly Pro Asp Ala Ala Ser Phe Arg
            450                 455                 460

ccg gag cgg tgg atc aac gag gat ggc gcg ttc cgc aac gcg tcg ccg      1440
Pro Glu Arg Trp Ile Asn Glu Asp Gly Ala Phe Arg Asn Ala Ser Pro
465                 470                 475                 480

ttc aag ttc acg gcg ttc cag gcg ggg ccg agg atc tgc ctg ggc aag      1488
Phe Lys Phe Thr Ala Phe Gln Ala Gly Pro Arg Ile Cys Leu Gly Lys
                485                 490                 495

gac tcg gcg tac ctg cag atg aag atg gcg ctg gcc atc ctc ttc cgc      1536
Asp Ser Ala Tyr Leu Gln Met Lys Met Ala Leu Ala Ile Leu Phe Arg
                500                 505                 510

ttc tac agc ttc cgg ctg ctg gag ggg cac ccg gtg cag tac cgc atg      1584
Phe Tyr Ser Phe Arg Leu Leu Glu Gly His Pro Val Gln Tyr Arg Met
                515                 520                 525

atg acc atc ctc tcc atg gcg cac ggc ctc aag gtc cgc gtc tct agg      1632
Met Thr Ile Leu Ser Met Ala His Gly Leu Lys Val Arg Val Ser Arg
            530                 535                 540

gcc gtc tga tgt cat ggc gat ttg gat atg gat atc gtc ccg ctt aat      1680
Ala Val     Cys His Gly Asp Leu Asp Met Asp Ile Val Pro Leu Asn
545                 550                 555
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cca cga caa ata acg c   gtg tta caa att tgc atg cat gca tgt aag      1728
Pro Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys
560             565             570             575

gga aag cga tgg gtt tca ttg gtg gct tgg ctt aag cct taaaaactcc       1777
Gly Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro
            580             585

gtcgggtctt gcgaaccacc acatcactag tgttttgtac tctactcctc agtggaagtg    1837

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<213> Zea mays

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Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys
        35              40              45

Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg
    50              55              60

Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His
65              70              75              80

Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala
            85              90              95

Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr
            100             105             110

Pro Lys Gly Ile Val Tyr Arg Ser Tyr Met Asp Val Leu Leu Gly Asp
        115             120             125

Gly Ile Phe Asn Ala Asp Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr
    130             135             140

Ala Ser Phe Glu Phe Ala Ser Lys Asn Leu Arg Asp Phe Ser Ala Ile
145             150             155             160

Val Phe Arg Glu Tyr Ser Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala
            165             170             175

Ser Lys Ala Gly Lys Val Val Asp Met Gln Glu Leu Tyr Met Arg Met
        180             185             190
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Thr Leu Asp Ser Ile (Lys Val Gly Phe Gly Val Glu Ile Gly Thr
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Leu Ser Pro Asp Leu Pro Glu Asn Ser Phe Ala Gln Ala Phe Asp Ala
      210   215   220

Ala Asn Ile Ile Ile Thr Leu Arg Phe Ile Asp Pro Leu Trp Arg Ile
225   230   235   240

Lys Arg Phe Phe His Val Gly Ser Glu Ala Leu Leu Ala Gln Ser Ile
           245   250   255

Lys Leu Val Asp Glu Phe Thr Tyr Ser Val Ile Arg Arg Arg Lys Ala
         260   265   270

Glu Ile Val Glu Val Arg Ala Ser Gly Lys Gln Glu Lys Met Lys His
       275   280   285

Asp Ile Leu Ser Arg Phe Ile Glu Leu Gly Glu Ala Gly Asp Asp Gly
     290   295   300

Gly Gly Phe Gly Asp Asp Lys Ser Leu Arg Asp Val Val Leu Asn Phe
305   310   315   320

Val Ile Ala Gly Arg Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Thr
         325   330   335

His Met Ala Met Ser His Pro Asp Val Ala Glu Lys Leu Arg Arg Glu
         340   345   350

Leu Cys Ala Phe Glu Ala Glu Arg Ala Arg Glu Glu Gly Val Thr Leu
      355   360   365

Val Leu Cys Gly Gly Ala Asp Ala Asp Asp Lys Ala Phe Ala Ala Arg
     370   375   380

Val Ala Gln Phe Ala Gly Leu Leu Thr Tyr Asp Ser Leu Gly Lys Leu
385   390   395   400

Val Tyr Leu His Ala Cys Val Thr Glu Thr Leu Arg Leu Tyr Pro Ala
           405   410   415

Val Pro Gln Asp Pro Lys Gly Ile Leu Glu Asp Asp Val Leu Pro Asp
         420   425   430

Gly Thr Lys Val Arg Ala Gly Gly Met Val Thr Tyr Val Pro Tyr Ser
         435   440   445

Met Gly Arg Met Glu Tyr Asn Trp Gly Pro Asp Ala Ala Ser Phe Arg
   450   455   460

Pro Glu Arg Trp Ile Asn Glu Asp Gly Ala Phe Arg Asn Ala Ser Pro
465   470   475   480

Phe Lys Phe Thr Ala Phe Gln Ala Gly Pro Arg Ile Cys Leu Gly Lys
        485   490   495

```
Asp Ser Ala Tyr Leu G.   Met Lys Met Ala Leu Ala Ile Leu Phe Arg
              500             505                 510
```

```
Phe Tyr Ser Phe Arg Leu Leu Glu Gly His Pro Val Gln Tyr Arg Met
        515             520             525
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```
Met Thr Ile Leu Ser Met Ala His Gly Leu Lys Val Arg Val Ser Arg
    530             535             540
```

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Ala Val Cys His Gly Asp Leu Asp Met Asp Ile Val Pro Leu Asn Pro
545             550             555             560
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```
Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys Gly
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Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro
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<210> 3
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<212> DNA
<213> Sorghum sp.

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<223> "n" bases may be a, t, c, g, other or unknown

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gatgtgctcc tcggtgacgg catattcaac gctgacggcg agctgtggag gaagcagagg 180
aagacggcga gtttcgagtt cgcctccaag aacctgaggg atttcagtgc caatgttttc 240
agagagtact ccctgaagct gtcgggcata ctgagtcagg catccaaggc aggcaaagtt 300
gttgacatgc aggaacttta catgaggatg acactggact cgatctgcaa ngttggggttc 360
ggggtcnana tcggcacgct gtcnccggat ctccccgaga acagcttcnc ccaagcgttc 420
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<210> 4
<211> 158
<212> PRT
<213> Sorghum sp.

<220>
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<223> "Xaa" may be any, other or unknown amino acid

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            20              25                  30
```

```
Arg Ser Tyr Met Asp V; . Leu Leu Gly Asp Gly Ile Phe Asn Ala Asp
        35                40                45
```

```
Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr Ala Ser Phe Glu Phe Ala
    50                55                60
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```
Ser Lys Asn Leu Arg Asp Phe Ser Ala Asn Val Phe Arg Glu Tyr Ser
65                70                75                80
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Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala Ser Lys Ala Gly Lys Val
                85                90                95
```

```
Val Asp Met Gln Glu Leu Tyr Met Arg Met Thr Leu Asp Ser Ile Cys
            100               105               110
```

```
Xaa Val Gly Phe Gly Val Xaa Ile Gly Thr Leu Ser Pro Asp Leu Pro
        115               120               125
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Glu Asn Ser Phe Xaa Gln Ala Phe Asp Ala Ala Asn Ile Ile Val Thr
    130               135               140
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Leu Arg Phe Ile His Pro Leu Trp Arg Ile Gln Lys Phe Phe
145               150               155
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<212> DNA
<213> Zea mays

<400> 5
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acgcaatgag agatctattc agacttacac tggatgccgc caacaaattc aacctttaga 240
ttttgatact gtcactccta ctttattcct tggttgggca acttccaata ggctcatgtt 300
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<213> Zea mays

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